

411USPHRM311.ST25
SEQUENCE LISTING

<110> Vogeli, Gabriel
Lind, Peter
Wood, Linda S.
Parodi, Luis A.

<120> Novel G Protein Coupled Receptor

<130> 411USPHRM311

<150> 60/165,838

<151> 1999-11-16

<150> 09/714,449

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<150> 60/198,568

<151> 2000-04-20

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<151> 2000-03-17

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<151> 2000-05-02

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<151> 2000-05-08

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<151> 2000-05-25

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<170> PatentIn version 3.0

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 ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca 180
 ggaactttcc ctgggcctct ctgggccaca attcctggcc gagagaaaga ggaggaatga 240
 ggtgagcacc ttcttcactc ctagggccat gtggtagagc tgcagtcgca cctccttctg 300
 ccaataggca tagatgagtg ggttgagcag ggagttgcc acgccagca gccacagga 360
 ccgttcagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat 420
 aaggaagggg gtccaggata gagcaaagct cccaatgaga acagacacag tacggagagc 480
 tttgaagtcg ctgggagtcg gtggggatcg ataacctcca gccatggctc ctgcatgttc 540
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 gacaaagagg agcatggctg ggaagaagcc aacgcaggag agggtcagca cgaagtgagg 660
 gtgaaataca gcaaagaagc tgcactgccc tttgtaggca gtctgctgga acatggggat 720
 tccgagtggg aggaagccaa tgaggtgaaga cactaaccac agcccggcaa tgcaggcccc 780
 ggccacgaac cactcatga tcttcaagta gcggaagggc tgcttgatgg caaggtacct 840
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 catccgcagg ctgcacaggg tcttctgtgt gggccgagaa gggctggaga gctggtctgt 960
 gagtaggcca gagatggcca caccaatcaa ggtgtcagcc acagccagat tcaaggtgaa 1020
 gcagagactg acaccatcat tcttgtggat caacagcagc acagccacag ccactagtgt 1080
 gttagtagca atgatgaggg aggccaggac agcaaggatc actccaaatg agaaagatga 1140
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 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp

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50

55

60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ser Val Leu Thr Val
85 90 95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145 150 155 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165 170 175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180 185 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
210 215 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
325 330 335

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gagcgtggcg gtgaaggctg cgaagcgcgg acgctcaggc tcgggcgga ggcgcagcga 180

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acaggacgcg aaggcgctgc tgtagccaag ccacgagcag ccaagtgcag cgcctgagaa 240
 ggccagcgac tgtccccagg cacagcccag cagcaggccg gcatagcgcg gtcgcaggcg 300
 tccggcgtag cgcagtggga agcccactgc cagccactgg tctgcgctca gcgccgccac 360
 gctcagcgcc gcgttgagcg ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc 420
 gggcgccgac ggtgtccgcc cgcgcatcac accgagcagc gtgaaggcca tgtccagcgc 480
 cgccagcagc aggtggccca gagacagatt caccaggagg acgcctgagg ctcgagtgcg 540
 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc 600
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 20 25 30
 Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val
 35 40 45
 Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe
 50 55 60
 Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala
 65 70 75 80
 Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala
 85 90 95
 Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe
 100 105 110
 Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu
 115 120 125
 Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu
 130 135 140
 Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu
 145 150 155 160
 Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala
 165 170 175
 Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu
 180 185 190
 Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met
 195 200 205
 Asp Thr Val Thr Met Lys Ala Leu Ala
 210 215

<210> 5
 <211> 222
 <212> DNA
 <213> Homo sapiens

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 ggaaaggaaa tctgtgtatt ttggctcact actgactatc tgttatgtac agcatctgta 120
 tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaagtc tgtaagtcga 180
 acacattaat ttatccccct tagaagatta tgtaaagta ta 222

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 <212> PRT
 <213> Homo sapiens

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 1 5 10 15
 Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp
 20 25 30
 Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr
 35 40 45
 Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile
 50 55 60
 Pro Leu Arg Arg Leu Cys Lys Cys Ile
 65 70

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 cagcggggac agggcgggtca ggagcagcag ccaggtccct gcacacgcgg ccaccgcgta 120
 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgtccac 180
 gctgatacag gtcattggtga ggatgctgga atacatgttt gcgtaaaagg ccacggtcac 240
 cacgttgcaa agcagcaccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg 300
 gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac 360
 cgacggggat ctgggccccca tgcgccggca cagcaccac agagagaaga ggttgcccgg 420
 gatgctgacc gccgccacca gcgagtacac cacgggcagg gccaccgcga tcgccgggtt 480
 ccgcagcatc tgcagcgtcg cgttgtc 507

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<212> PRT
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 Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn
 20 25 30
 Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro
 35 40 45
 Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
 50 55 60
 Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
 65 70 75 80
 Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
 85 90 95
 Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg
 100 105 110
 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
 115 120 125
 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
 130 135 140
 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
 145 150 155 160
 Leu Gly Ile Ile Thr Cys Phe Asp Val
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 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgetgagcct cctgggcac 180
 gcgctggagc gcagcctcac catggcgcg cagggggccc cgcccgtctc cagtcggggg 240
 cgcacgctgg cgatggcagc cgcggcctgg 270

<210> 10
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 10

Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala
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Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu
 20 25 30

Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val
 35 40 45

Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg
 50 55 60

Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly
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Arg Thr Leu Ala Met Ala Ala Ala Ala Trp
 85 90

<210> 11
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 gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 180
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc 240
 gggagcatcg tgttccttac ggtggtggct gcggacaggt atttcaaagt ggtccacccc 300
 caccacgcgg tgaacactat ctccaccggg gtggcggctg gcacgtctg caccctgtgg 360
 gccctggtca tccctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 420
 acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg 480
 ttccagctgg agttctttat gccctcggc atcatcttat ttgctcctt caagattggt 540
 tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgaccgg 600
 ttcatcatgg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 660
 ctctatttcc tctggacggt gccctcgagt gctgcgac cctctgtcca tggggccctg 720
 cacataaccc tcagcttcac ctacatgaac agcatgctgg atccccctgt gtattatttt 780
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 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcg 888

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 <212> PRT
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Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val
 20 25 30

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Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu
 35 40 45

Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly
 50 55 60

Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala
 65 70 75 80

Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys
 85 90 95

Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala
 100 105 110

Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val
 115 120 125

Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser
 130 135 140

Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met
 145 150 155 160

Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser
 165 170 175

Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln
 180 185 190

Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val
 195 200 205

Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu
 210 215 220

Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu
 225 230 235 240

His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu
 245 250 255

Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu
 260 265 270

Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln
 275 280 285

Arg Pro Glu Glu Met Pro Ile Ser
 290 295

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tgcaagctgg tgcacttcct gttctatata aacctttacg gcagcatcct gctgctgacc 180

tgcatctctg tgcaccagtt cctaggtgtg tgccaccac tgtgttcgct gccctaccgg 240

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 ctgcccacac tggccttctc ccacacggac tacatcaatg gccagatgat ctggtatgac 360
 atgaccagcc aagagaattt tgatcggtt tttgcctacg gcatagttct gacattgtct 420
 ggctttcttt ccctccttgg tcattttggt gtgctattca ctgatgttca ggagcctgat 480
 caagccagag gagaacctca tgaggacagg 510

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Trp Ser Cys Ala Thr Thr Tyr Leu Val Asn Leu Met Val Ala Asp Leu
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Leu Tyr Val Leu Leu Pro Phe Leu Ile Ile Thr Tyr Ser Leu Asp Asp
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Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe
 35 40 45

Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val
 50 55 60

His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg
 65 70 75 80

Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val
 85 90 95

Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile
 100 105 110

Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp
 115 120 125

Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser
 130 135 140

Leu Leu Gly His Phe Gly Val Leu Phe Thr Asp Gly Gln Glu Pro Asp
 145 150 155 160

Gln Ala Arg Gly Glu Pro His Glu Asp Arg
 165 170

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 <222> (431)..(461)
 <223> n is any nucleotide

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cagcagctgg ctcatcttca ggctctgcac cttggcgcg ggcacgcgc tgggcgcacg 180
ggctccacct gggctcgccg accaggccgc tgcacccgct ggggccttca gccggtgccg 240
ccaccagacg gagagtaggt ggccacaagc gacacccatg atcttaacag gcgcgacgaa 300
gcccgcgacg gctcataga acgcgtacac ctgcacgtgc cagcgctgca ggagcgcgaa 360
gatccagtgg cagcgacgca tccccggcca ggctcgggcg gagagtggcg cgcctggctg 420
cagagacgtt nnnnnnnnnn nnnnnnnnnn nnnnnnnnn nagtactagc gcaccacaaa 480
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gggcagcggc cggccgtgcg gaagacgcac cgcgcgccgg cgctcgaggg cgatgagcac 600
cacgaggtgg gccgaggcgc cccgcccgga tgctgcagc agctgcagga agcggcacgc 660
caggtecccc gtggccgcgc ggggctcgcc cagcagttcc caggccagct gtgacagcgc 720
cgtgcccccg cacgcgtaca ggtccgccag ggccagctgc accagcagga agtccatctt 780
gcgacgcttn nnnnnnnnnn nnnnnnnnnn nnnnnnnnac aggcggcaca gcaactgtggt 840
gttgctgcc accgccacca ccaggatgac cccaggaac accaggcgga cgcg 894

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<222> (26)..(35)
<223> Xaa is unknown

<220>
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<223> Xaa is Unknown

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20 25 30
Xaa Xaa Xaa Lys Arg Arg Lys Met Asp Phe Leu Leu Val Gln Leu Ala
35 40 45
Leu Ala Asp Leu Tyr Ala Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala
50 55 60
Trp Glu Leu Leu Gly Glu Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys
65 70 75 80
Arg Phe Leu Gln Leu Leu Gln Ala Ser Gly Arg Gly Ala Ser Ala His
85 90 95

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Leu Val Val Leu Ile Ala Leu Glu Arg Arg Arg Ala Val Arg Leu Pro
 100 105 110
 His Gly Arg Pro Leu Pro Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu
 115 120 125
 Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe Val Val Arg Tyr Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Leu Gln Pro Gly
 145 150 155 160
 Ala Pro Leu Ser Ala Arg Ala Trp Pro Gly Met Arg Arg Cys His Trp
 165 170 175
 Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr
 180 185 190
 Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala
 195 200 205
 Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro
 210 215 220
 Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro
 225 230 235 240
 Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu
 245 250 255
 Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu
 260 265 270
 Glu Ala Ala Trp Ser Ser Gly Pro Ala Gly Glu Trp Glu Gly Glu Ala
 275 280 285
 Leu Ser Ala Cys Cys Ala Trp Trp
 290 295

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 ggggaggagg tagaatagga aggaggtgac ctggatgatg aaattgtaga tccacatggg 180
 cttgatgacc gtacaggtgg ccgaacctgg gaccagggac ccattgggga agtagtgga 240
 cttgatgcca tggatgctgg tgttgggcag ggagaagagc acggagaagc cccagacgat 300
 gccgaggatc ctgagggccc ggcgccgggt gctctgcagt ttggcgcgga acgggtgtag 360
 gatggccacg tagcgctcca cgctgacggt ggtgatgctg aggatggagg cgaagcacac 420
 ggtctcaaag agggccgtct tgaagtagca gccacgggc ccgaacaaga aagggtagtt 480
 gcgccacatc tcatagacct ccaggggcat tccaaggagc aggaccagga ggtagagac 540
 cgccaggctg aagaggtagt agttggtggg cgtcttcata gcctggtgct gcagaatcac 600

caggcacacc aggacattgc caatgacccc caccacaaaa attggcacat acaccacaga 660
 caccggggagg aagaagtggc tgcgccgagg tccgcagagg aaggccagat actcctcggg 720
 gctgttcagg tgtttctgga atggatcttc tagtttctgc tggtagatcc aggaagcatt 780
 ctgaagtttt tccatccctg a 801

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<400> 18

Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
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 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
 35 40 45
 Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
 50 55 60
 Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Asn Thr
 65 70 75 80
 Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
 85 90 95
 Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
 100 105 110
 Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
 115 120 125
 Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
 130 135 140
 Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
 145 150 155 160
 Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe
 165 170 175
 Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro
 180 185 190
 Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro
 195 200 205
 Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr
 210 215 220
 Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu
 225 230 235 240
 Arg Val Ser Ile Ala Gly Val Ala Gly
 245

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 <213> Homo sapiens

<400> 19
 atcaagatga tttttgctat cgtgcaaatt attggatttt ccaactccat ctgtaatccc 60
 attgtctatg cttttatgaa tgaaaacttc aaaaaaatg ttttgtctgc agtttggtat 120
 tgcataagtaa ataaaacctt ctctccagca caaaggcatg gaaattcagg aattacaatg 180
 atgcggaaga aagcaaagtt ttccctcaga gagaatccag tg 222

<210> 20
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 20
 Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
 1 5 10 15
 Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
 20 25 30
 Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
 35 40 45
 Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
 50 55 60
 Ala Lys Phe Ser Leu Arg Glu Asn Pro
 65 70

<210> 21
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 21
 gccacagcat gcagttttct gtagaattcc actttgtctt tgcacttgaa gaagatgagg 60
 tatctggtga ccaggatcac cacatagaat aggaaccgtg aggtacatgt ggatgtgcag 120
 catggcactc acaaatttgc agaagggcag cccaaacatc caagtcttct tgatgaggta 180
 ggtaagcga aatggcactg tcagcagaaa aacgctgtgg accaccacca agttaatgac 240
 cgccatggtg gtcactgacc ggggtgttcat tttcaccagg aggaaaagaa tggaaatgac 300
 acccaccagc ccgccaataa gcactatgaa gtagaggctg attaagtggg gtgtcactat 360
 aggatcgcaa gaggaattcc tggaggtatt gtggccaggc atacttgga agtcacctgg 420
 aggagaaaaa gcaccagagt aactgac 447

<210> 22
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 22

Val Ser Tyr Ser Gly Ala Phe Ser Pro Pro Gly Asp Phe Pro Ser Met
 1 5 10 15
 Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
 20 25 30
 Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
 35 40 45
 Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
 50 55 60
 Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
 65 70 75 80
 Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
 85 90 95
 Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
 100 105 110
 His Met Tyr Leu Thr Val Pro Ile Leu Cys Gly Asp Pro Gly His Gln
 115 120 125
 Ile Pro His Leu Leu Gln Val Gln Arg Gln Ser Gly Ile Leu Gln Lys
 130 135 140
 Thr Ala Cys Cys Gly
 145

<210> 23

<211> 222

<212> DNA

<213> Homo sapiens

<400> 23

actgaccaag gtcagggcat cgactgaggg tagaaggcca caggaaatgc cagtcaaggt 60
 gttggcgcct gcaatcgcac ctaccacaaa cttgaccggg ggcagggggg caggcccgcc 120
 agcgaacacg gtcagcagca ccagtcatt gcagagcacg gagagcaaca cgatggccca 180
 cacggccagg cggatgcccc agctttcaaa gaggtactca ca 222

<210> 24

<211> 74

<212> PRT

<213> Homo sapiens

<400> 24

Cys Glu Tyr Leu Phe Glu Ser Trp Gly Ile Arg Leu Ala Val Trp Ala
 1 5 10 15
 Ile Val Leu Leu Ser Val Leu Cys Asn Gly Leu Val Leu Leu Thr Val
 20 25 30
 Phe Ala Gly Gly Pro Ala Pro Leu Pro Pro Val Lys Phe Val Val Gly
 35 40 45
 Ala Ile Ala Gly Ala Asn Thr Leu Thr Gly Ile Ser Cys Gly Leu Leu
 50 55 60

Ala Ser Val Asp Ala Leu Thr Leu Val Ser
65 70

<210> 25
<211> 246
<212> DNA
<213> Homo sapiens

<400> 25
aaccatca tctacacgct caccaaccgc gacctgcgcc acgcgctcct gcgcctggtc 60
tgctgcggac gccactcctg cggcagagac ccgagtggct ccagcagtc ggcgagcgcg 120
gctgaggctt ccgggggcct gcgcgcgtgc ctgcccccg gccttgatgg gagcttcagc 180
ggctcggagc gctcatcgcc ccagcgcgac gggctggaca ccagcggctc cacaggcagc 240
cccggt 246

<210> 26
<211> 82
<212> PRT
<213> Homo sapiens

<400> 26
Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu
1 5 10 15
Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser
20 25 30
Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg
35 40 45
Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg
50 55 60
Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser
65 70 75 80
Pro Gly

<210> 27
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (81)..(106)
<223> n is any nucleic acid

<400> 27
cgtgaagaac agcgcaccca tgaccagcat gtgcaccacg cgcgctctgc gccgcgatgc 60
tcgcgggtcc gcagcctcct nnnnnnnnnn nnnnnnnnnn nnnnnntggc agagcttgcg 120
cgcgatgcgg gcgtacatga ccagcatgag cgccagcggc gccaggtaga tgtgcgagaa 180
gagcacagtg gtgtagacct tgcgcatgcc cttctcgggc caggcctccc agcaggagta 240

411USPHRM311.ST25

gagagggtag gagcggttgc gggcggtccac catgaagtgg tgctcctcac gggtgacggt 300
cagcgtgacg gccgaggac acatgatgag cagcgccagg gccagatga cggcgatggt 360
gacgagcgcc ttccgcaggg tcagcttctc gcggaaaggg tgcacgatgc agcggaacct 420

<210> 28
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (104)..(113)
<223> Xaa is Unknown

<400> 28

Phe Arg Cys Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys
1 5 10 15
Ala Leu Val Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met
20 25 30
Cys Pro Ser Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe
35 40 45
Met Val Asp Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu
50 55 60
Ala Trp Pro Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe
65 70 75 80
Ser His Ile Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala
85 90 95
Arg Ile Ala Arg Lys Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110
Xaa Glu Ala Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val
115 120 125
His Met Leu Val Met Val Ala Leu Phe Phe Thr
130 135

<210> 29
<211> 318
<212> DNA
<213> Homo sapiens

<400> 29
gcagggggcg tgagtcctca ggcacttctt gaggtccttg ttgagcagga agcagacaat 60
tgggttgacg gcagcctggg cgaagctcat ccaaacagca gtggccaggt agcggtgggg 120
cacagcacag gctttcacaa aactcgcca gtagcaggcc acgatgtagg gtgaccagag 180
gagcagaaaag agcagtgtga tcgcgtagaa catgcggccc agctgctttt cacccttgac 240
ctcgtccatg cccagtagcc gccggctggc tgcattgcca ttctgccgga taccagcag 300
ggttggtggc atggggccc 318

<210> 30
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 30

Gly Pro Met Pro Pro Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala
 1 5 10 15
 Ala Ser Arg Arg Leu Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln
 20 25 30
 Leu Gly Arg Met Phe Tyr Ala Ile Thr Leu Leu Phe Leu Leu Trp
 35 40 45
 Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys
 50 55 60
 Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala
 65 70 75 80
 Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu
 85 90 95
 Lys Lys Cys Leu Arg Thr His Ala Pro Cys
 100 105

<210> 31
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 31
 tattctgtaa tgaagaatgt cattcacact gccattggca catccagtgg cctcacctag 60
 cattgtgaaa gcccttcggt tgggtgtattg ccacttcatt ttaaaaggat gcacaagtcc 120
 ctggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacia cagcggtaga 180
 ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatc 240
 atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgtaattat cactatcagt 300
 ccattctgag cctctgccaa aaagtttgat aattgtaatt actctgtaga caca 354

<210> 32
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu
 1 5 10 15
 Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu
 20 25 30
 Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe
 35 40 45

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Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu
50 55 60

Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val
65 70 75 80

His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr
85 90 95

Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile
100 105 110

Leu His Tyr Arg Ile
115

<210> 33
<211> 621
<212> DNA
<213> Homo sapiens

<400> 33
gagcaacatg atctttttga agtacttgac ggtgtcggtc ttgacggtca cgaagcacag 60
agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagtgaggta 120
gtgcttctcc ttcacaaaca cgggtgggaa gaagtcgagc acgatggtga agccgtagaa 180
gggcgcccag catagcacgt aggcggtgag gatgcacatg agcaccagga ccgtcttcct 240
gcggcagcgc agcctcttgc ggatctgctc tgtctggaat ccagggaccg ccttgaacca 300
gagctcccgg gagatcctgg catagcacag ggtcatggtg accacggggc ccacgaattc 360
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420
ctggccgcag aagatctttt cctggctctt gacaatgacg aggaccgtct cgggtggtgaa 480
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540
ggctgttttg cacttcattc gtggtctcag cggatggaca atagccagat acctagggca 600
agaacacaag tggaggcagc c 621

<210> 34
<211> 207
<212> PRT
<213> Homo sapiens

<400> 34

Gly Cys Leu His Leu Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His
1 5 10 15

Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala
20 25 30

Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe
35 40 45

Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe
50 55 60

Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr
65 70 75 80

Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met
 85 90 95
 Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val
 100 105 110
 Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg
 115 120 125
 Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys
 130 135 140
 Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr
 145 150 155 160
 Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu
 165 170 175
 Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr
 180 185 190
 Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu
 195 200 205

<210> 35
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 35
 cagccacact gcagtgatga aatcaaatgt ccaacaccaa ccatagtcac cattactaac 60
 taagaagcca caaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120
 ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180
 gacagacagg cagcactcag tactgatggc actcagcatg ctcaggccta caaggtaggc 240
 aaagggtcatc acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300
 actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggccccggc 360
 caggctgagg acgtagacag agaaggcggt cctgcgcatg cggaagccca ggagccagag 420
 cacaaacccg tttcctacca gcccgaccag ggcaatgaaa aggatcagga agaccgggat 480
 cag 483

<210> 36
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val
 1 5 10 15
 Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn
 20 25 30
 Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe
 35 40 45

Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe
 50 55 60
 Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr
 65 70 75 80
 Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu
 85 90 95
 Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro
 100 105 110
 Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu
 115 120 125
 Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn
 130 135 140
 Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp
 145 150 155 160
 Leu

<210> 37
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 37
 gagagtctga ttctgactta catcacatat gtaggcctgg gcatttctat ttgcagcctg 60
 atccttttgct tgtccgttga ggtcctagtc tggagccaag tgacaaagac agagatcacc 120
 tatttacgcc atgtgtgcat tgttaacatt gcagccactt tgctgatggc agatgtgtgg 180
 ttcatgttgg ctctctttct tagtggccca ataacacacc acaagggatg tgtggcagcc 240
 acattttttg gtcatttctt ttacctttct gtatttttct ggatgcttgc caaggcactc 300
 cttatcctct atggaatcat gattgttttc 330

<210> 38
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 38

Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser
 1 5 10 15
 Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser
 20 25 30
 Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val
 35 40 45
 Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala
 50 55 60
 Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala
 65 70 75 80

Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu
 85 90 95

Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe
 100 105 110

<210> 39
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 39
 ttgtgtggca gtagagagat gtcaggcttc agagtcaaca agaactggat ttcaaactgg 60
 atttgaggac cccacaccttt ggtaagtgac ttattatctg cgagcctctg tttctctctt 120
 ctttaaataa ggacagtaaa tcccatcacg caggggtggtg gggagaatca gagatgatac 180
 agctggtgat cacatctggt ttgtgttccc aggggcacca gactagggtt tctgagcatg 240
 gatccaaccg tcccagtctt cggtaaaaa ctgacaccaa tcaacggacg tgaggagact 300
 ccttgctaca atcagaccct gagcttcacg gtgctgacgt gcatcatttc ccttgctcga 360
 ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgcag gaacgctgtc 420
 tccatctaca tcctcaacct ggccgcagca gacttcctct tcctcagctt ccagattata 480
 cgttcgccat tacgcctcat caatcacgc catctcatcc gcaaaatcct cgtttctgtg 540
 atgacctttc cctactttac aggcctgagt atgctgagcg ccatcagcac cgagcgctgc 600
 ctgtctgttc tgtggcccat ctggtacc 628

<210> 40
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 40
 Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp
 1 5 10 15
 Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser
 20 25 30
 Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg
 35 40 45
 Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys
 50 55 60
 Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val
 65 70 75 80
 Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr
 85 90 95
 Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile
 100 105 110
 Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly

115

120

125

Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala
 130 135 140

Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu
 145 150 155 160

Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val
 165 170 175

Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser
 180 185 190

Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
 195 200 205

<210> 41

<211> 319

<212> DNA

<213> Homo sapiens

<400> 41

acagaaagca aggccaccag gaccttaggc atagtcattg gagtggttgt gttgtgctgg 60

ctgcccttct ttgtcttgac gatcacagat cctttcatta attttacaac ccttgaagat 120

ctgtacaatg tcttcctctg gctaggctat ttcaactctg ctttcaatcc cattttatat 180

ggcatgcttt atccttggtt tcgcaaggca ttgaggatga ttgtcacagg catgatcttc 240

caccctgact cttccaccct aagcctgttt tctgcccattg cttaggctgt gttcatcatt 300

caataggact cttttctgg 319

<210> 42

<211> 103

<212> PRT

<213> Homo sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe
 1 5 10 15

Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe
 20 25 30

Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu
 35 40 45

Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr
 50 55 60

Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe
 65 70 75 80

His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val
 85 90 95

Phe Ile Ile Gln Asp Ser Phe
 100

<210> 43

<211> 515
 <212> DNA
 <213> Homo sapiens

<400> 43
 taggaatctc agagaagaaa gtaaggaacc agaaaacat aaaagaatgt aaatggaaaa 60
 gaatcagcaa atcttattca cttatcacta aatctaaaat atgtcaaaat acatgaagac 120
 aacaaatgct ttagaacaac tgttgaatgt attgtcctac aacttggcat atgatcatgc 180
 ttgcctctct atgtccaagt gtttattttt gcagttgacc ttaatttcaa gttagttttg 240
 aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagtgtgt 300
 gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaacat 360
 tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420
 aaaatctcat aaacataagg aggagtata aaattcatat aagcatcaat cactgcatca 480
 acgaggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 44
 Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala
 1 5 10 15
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala
 20 25 30
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp
 35 40 45
 Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe
 50 55 60
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val
 65 70 75 80
 Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu
 85 90 95
 Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg
 100 105 110
 Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met
 115 120 125
 Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu
 130 135 140
 Ser Ser Cys Ile
 145

<210> 45
 <211> 726
 <212> DNA
 <213> Homo sapiens

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<400> 45
ctggaaagag gtcctcgatc taccctctac gccgtccttg gttttggggc tgtgctggca    60
gcgttttgaa acttactggt catgattgct atccttcact tctaacaact gcacacacct    120
acaaactttc tgattgcgtc gctggcctgt gctgacttct tggtagggagt cactgtgatg    180
cccttcagca cagtggaggtc tgtggagagc tgttggtact ttggggacag ttactgtaaa    240
ttccatacat gttttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc    300
tctgttgata gatacattgc tgttactgat cctctgacct atccaaccaa gtttactgtg    360
tcagtttcag ggatatgcat tgttctttcc tggttctttt ctgtcacata cagcttttcg    420
atcttttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt    480
gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc    540
tttataacca atgtcgccat ggtgtttata tacagtaaga tatttttggg ggccaagcat    600
caggctagga agatagaaaag tacagccagc caagctcagt ccttctcaga gagttacaag    660
gaaagagtag caaaaagaga gagaaaggct gccaaaacct tgggaattgc tatggcagca    720
tttctt                                     726

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<210> 46
<211> 241
<212> PRT
<213> Homo sapiens

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<400> 46

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Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly
1          5          10          15
Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu
20          25          30
His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala
35          40          45
Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val
50          55          60
Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe
65          70          75          80
His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu
85          90          95
Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr
100         105         110
Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu
115         120         125
Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly
130         135         140
Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val
145         150         155         160

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Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe
 165 170 175
 Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys
 180 185 190
 Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala
 195 200 205
 Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys
 210 215 220
 Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe
 225 230 235 240
 Leu

<210> 47
 <211> 660
 <212> DNA
 <213> Homo sapiens

<400> 47
 aaccaggtgg ccttactcct aagacccttg gccttgctta tggcctttat caacagctgt 60
 ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120
 ctgctagctg ccttagaacg ggcacttagc gaggagccag atagtgcctg aatcccagct 180
 cccaggcaga tgagtccttt ataacatgac ccaatttcct actccatttt cccaccactc 240
 aatcctcttc ccaaacagct ctaccataat ccaacatcca acagaattta agagaataaa 300
 ccacaacttt taagtgaact ctatgtgcta ggtcatgttt tagaatacaa ccttaagtgc 360
 ctggaagatg gaggaagaa acaaacaagg tctcattctt tagaggaaga cagttcacca 420
 agactcaaac agaaaaaag atagtatatc tgtgacaaaa caagtcataa aattgggtca 480
 ggacctgcag caatgacttt atgctagaat ccagagcact agcaggaaac tgcttaaatt 540
 ttacttaatc aaagtcaagt ttggacatac atgtcaggta aaacctagca gagatgagct 600
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<210> 48
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 48

Asn Gln Val Ala Leu Leu Leu Arg Pro Leu Ala Leu Ser Met Ala Phe
 1 5 10 15
 Ile Asn Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Ile Gly His Asp
 20 25 30
 Phe Trp Glu His Leu Leu His Ser Leu Leu Ala Ala Leu Glu Arg Ala
 35 40 45
 Leu Ser Glu Glu Pro Asp Ser Ala Ile Pro Ala Pro Arg Gln Met Ser

50

55

60

Pro Leu His Asp Pro Ile Ser Tyr Ser Ile Phe Pro Pro Leu Asn Pro
65 70 75 80

Leu Pro Lys Gln Leu Tyr His Asn Pro Thr Ser Asn Arg Ile Glu Asn
85 90 95

Lys Pro Gln Leu Leu Ser Glu Leu Tyr Val Leu Gly His Val Leu Glu
100 105 110

Tyr Asn Leu Lys Cys Leu Glu Asp Gly Gly Lys Lys Gln Thr Arg Ser
115 120 125

His Ser Leu Glu Glu Asp Ser Ser Pro Arg Leu Lys Gln Lys Lys Arg
130 135 140

Leu Ser Cys Asp Lys Thr Ser His Lys Ile Gly Ser Gly Pro Ala Ala
145 150 155 160

Met Thr Leu Cys Asn Pro Glu His Gln Glu Thr Ala Ile Leu Leu Asn
165 170 175

Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr
180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe
195 200 205

Asp Asp Leu
210

<210> 49
<211> 465
<212> DNA
<213> Homo sapiens

<400> 49
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ccccaacaa cttcgtgctc ctggcgaca tcgtgagccg cctgttctac ggcaagagct 180
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gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctcttctcc gccaggacca 360
cgtccgtgcg ctccgaggcc ggtgcgcacc ctgaagggat ggaggagacc accaggcccg 420
gcctccagag gcaggagagt gtgttctgag tccgggggc gcagc 465

<210> 50
<211> 160
<212> PRT
<213> Homo sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His
1 5 10 15

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Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu
20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala
35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr
50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe
65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr
85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu
100 105 110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala
115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln
130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg
145 150 155 160

<210> 51

<211> 603

<212> DNA

<213> Homo sapiens

<400> 51

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ccggaacca cagggccccc tgggccatga gaggctcctg gacttgaacc tcaggacact 180

cccactctgg ctgccggcag ggatggaagc tggatgagca ggcaggagct ggcagtgggg 240

gtggagagcc ataggctatt ggggtggaca ggcttgggtg cctcatggga gctcccatg 300

ggagctgtgg ccccttgggg cctcttattt ctcacccag gctttcccg gagaggttca 360

agtcagaaga tgcccaaag atccacgtgg ccctgggtgg cagcctgttc ctctgaatc 420

tggccttctt ggtcaatgtg gggagtggct caaaggggtc tgatgctgcc tgctgggccc 480

ggggggctgt cttccactac ttctgctct gtgccttcac ctggatgggc ctggaagcct 540

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agc 603

<210> 52

<211> 198

<212> PRT

<213> Homo sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser
1 5 10 15

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Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile
 20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp
 35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys
 50 55 60

Arg Gln Gly Trp Lys Leu Asp Glu Gln Ala Gly Ala Gly Ser Gly Gly
 65 70 75 80

Gly Glu Pro Ala Ile Gly Val Asp Arg Leu Gly Cys Leu Met Gly Ala
 85 90 95

Pro His Gly Ser Cys Gly Pro Leu Gly Pro Leu Ile Ser His Pro Arg
 100 105 110

Leu Ser Arg Glu Arg Phe Lys Ser Glu Asp Ala Pro Lys Ile His Val
 115 120 125

Ala Leu Gly Gly Ser Leu Phe Leu Leu Asn Leu Ala Phe Leu Val Asn
 130 135 140

Val Gly Ser Gly Ser Lys Gly Ser Asp Ala Ala Cys Trp Ala Arg Gly
 145 150 155 160

Ala Val Phe His Tyr Phe Leu Leu Cys Ala Phe Thr Trp Met Gly Leu
 165 170 175

Glu Ala Phe His Leu Tyr Leu Leu Ala Val Arg Val Phe Asn Thr Tyr
 180 185 190

Phe Gly His Tyr Phe Leu
 195

<210> 53
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 53
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 gcgagaaggg gatttttcaca caggacccat tcacgttcgc gtagcacagc tgcacagcca 180
 ccagcaggga tgaattgctg ctcataacgc tggatattac atatggagaa attttgcct 240
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 acacatatcc accaggatgc cagaggaaat gatca 335

<210> 54
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 54

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly
 1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys
 20 25 30
 Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser
 35 40 45
 Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser
 50 55 60
 Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile
 65 70 75 80
 Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val
 85 90 95
 Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn
 100 105 110

<210> 55
 <211> 586
 <212> DNA
 <213> Homo sapiens

<400> 55
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 tatcctgaac ttcgtctatc caactgctta tatatgttca gaaaacaaat tcatggttgc 180
 tgaactgttc tttaaaacct gaccagttac aataactttt attgctttcc taaaccatgg 240
 gtaaaataaa gcataaatca aaggattcat ggctgagtta taataagcac accaacagca 300
 tcataaatac aggcaggggt tataaagccc ataaaggcat caattaatga atcaatgcta 360
 tatggtaacc atgaaatcat aaatgctacc actgtgaccc ccagggtttt agctgctttt 420
 ctctctctcc tggccactct ggctttgtaa ctctctgagg atgattctgt cttgctacca 480
 gtattttcta tctttttcgc ctgtcgtcta gccacaagaa atatgttacc atacagaatt 540
 atcataataa aggtaggtat aaagaaggat agaaaatctg tcaaca 586

<210> 56
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 56

Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile
 1 5 10 15
 Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile
 20 25 30
 Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala
 35 40 45
 Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr
 50 55 60

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Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu
65 70 75 80

Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile
85 90 95

Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr
100 105 110

Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr
115 120 125

Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu
130 135 140

His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser
145 150 155 160

Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys
165 170 175

Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val
180 185 190

<210> 57
<211> 976
<212> DNA
<213> Homo sapiens

<400> 57
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ctgtctacgt cctcagcctg gccggggccg acttcctctt cctctgcttc cagattataa 180
attgcctggt gtacctcagt aacttcttct gttccatctc catcaatttc cctagcttct 240
tcaccactgt gatgacctgt gcctaccttg caggcctgag catgctgagc accgtcagca 300
ccgagcgctg cctgtccgtc ctgtggccca tctggtatcg ctgccgccgc cccagacacc 360
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ggaagtctctg tggcttctta tttagtgtg gtgactctgg ttggtgtcag acatttgatt 480
tcatcactgc agcgtggctg atttttttat tcatggttct ctgtgggtcc agtctggccc 540
tgctgggtcag gatcctctgt ggctccaggg gtctgccact gaccaggctg tacctgacca 600
tctgtctcac agtgtggtg tccctctctt gggcctgcc ctttggcatt cagtggttcc 660
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gaggcaactt tgcccc 976

<210> 58
 <211> 324
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (266)..(266)
 <223> Xaa is Unknown

<400> 58

Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
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Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
 20 25 30

Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
 35 40 45

Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
 50 55 60

Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
 65 70 75 80

Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
 85 90 95

Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
 100 105 110

Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
 115 120 125

Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
 130 135 140

Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
 145 150 155 160

Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
 165 170 175

Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
 180 185 190

Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Ser Leu
 195 200 205

Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
 210 215 220

Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
 225 230 235 240

Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
 245 250 255

Val Gly Ser Phe Arg Lys Gln Trp Arg Xaa Gln His Pro Ile Leu Lys
 260 265 270

Leu Ala Leu Gln Arg Ala Leu Gln Asp Ile Ala Glu Val Asp His Ser

275

280

285

Glu Gly Cys Phe Arg Gln Gly Thr Arg Arg Phe Lys Glu Ala Phe Trp
 290 295 300

Cys Arg Asp Gly Pro Leu Tyr Phe His His Ile Tyr Val Ala Leu Arg
 305 310 315 320

Gly Asn Phe Ala

<210> 59

<211> 578

<212> DNA

<213> Homo sapiens

<400> 59

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 gccttcgtgc tttctgctta aggcagctgt cagtttgagc tccatggggtc aaagtgtgga 300
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 aaatcaggtt gtaccactta atagtattga gttcatccga actgggtgagg tcgagacagg 420
 ctgatctgtt ggtcctgttg gttgatgtga tcaagaaggt catcggaatg acagctacca 480
 gtgaaatgat ccacaccaca gcacaggcta caactgcaca tcgagttttg tgaatggaaa 540
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<210> 60

<211> 192

<212> PRT

<213> Homo sapiens

<400> 60

Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His
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Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser
 20 25 30

Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg
 35 40 45

Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn
 50 55 60

Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu
 65 70 75 80

Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu
 85 90 95

Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg
 100 105 110

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Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe
 115 120 125
 His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser
 130 135 140
 Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp
 145 150 155 160
 His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 165 170 175
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
 180 185 190

<210> 61
 <211> 872
 <212> DNA
 <213> Homo sapiens

<400> 61
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 tcttttctcat cccctccatt tctgtgtcaa tctcaatcca tttatatcgg tggccacttt 180
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<210> 62
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 62

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 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60
 Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
 65 70 75 80
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Glu
 130 135 140

<210> 63
 <211> 962
 <212> DNA
 <213> Homo sapiens

<400> 63
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 tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180
 aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca 240
 aagggaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300
 taatatttcc tgtgtgaaaa acaactgggc aaatgatgtc cgtgcttccc tgtacagttt 360
 aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc 420
 acacttcaaa caacttcata cccaacaaa ttggctcatt cattccatgg ccaactgtgga 480
 ctttcttctg ggggtgtctg tcatgcctta cagtatgggt agatctgctg agcactgttg 540
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 ctccattttc catttgtctt tcatctccat tgaccgtac tatgctgtgt gtgatccact 660
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<210> 64
 <211> 238

<212> PRT
 <213> Homo sapiens

<400> 64

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		20						25					30			
Ala	Ser	Leu	Tyr	Ser	Leu	Met	Val	Leu	Ile	Ile	Leu	Thr	Thr	Leu	Val	
		35					40					45				
Gly	Asn	Leu	Ile	Val	Ile	Val	Ser	Ile	Ser	His	Phe	Lys	Gln	Leu	His	
	50					55					60					
Thr	Pro	Thr	Asn	Trp	Leu	Ile	His	Ser	Met	Ala	Thr	Val	Asp	Phe	Leu	
65					70					75					80	
Leu	Gly	Cys	Leu	Val	Met	Pro	Tyr	Ser	Met	Val	Arg	Ser	Ala	Glu	His	
			85						90					95		
Cys	Trp	Tyr	Phe	Gly	Glu	Val	Phe	Cys	Lys	Ile	His	Thr	Ser	Thr	Asp	
			100					105						110		
Ile	Met	Leu	Ser	Ser	Ala	Ser	Ile	Phe	His	Leu	Ser	Phe	Ile	Ser	Ile	
		115					120					125				
Asp	Arg	Tyr	Tyr	Ala	Val	Cys	Asp	Pro	Leu	Arg	Tyr	Lys	Ala	Lys	Met	
	130					135					140					
Asn	Ile	Leu	Val	Ile	Cys	Val	Met	Ile	Phe	Ile	Ser	Trp	Ser	Val	Pro	
145					150					155					160	
Ala	Val	Phe	Ala	Phe	Gly	Met	Ile	Phe	Leu	Glu	Leu	Asn	Phe	Lys	Gly	
				165					170					175		
Ala	Glu	Glu	Ile	Tyr	Tyr	Lys	His	Val	His	Cys	Arg	Gly	Gly	Cys	Ser	
			180					185					190			
Val	Phe	Phe	Ser	Lys	Ile	Ser	Gly	Val	Leu	Thr	Phe	Met	Thr	Ser	Phe	
		195					200					205				
Tyr	Ile	Pro	Gly	Ser	Ile	Met	Leu	Cys	Val	Tyr	Tyr	Arg	Ile	Tyr	Leu	
	210					215					220					
Ile	Ala	Lys	Glu	Gln	Ala	Arg	Leu	Ile	Ser	Asp	Ala	Asn	Gln			
225					230					235						

<210> 65
 <211> 1018
 <212> DNA
 <213> Homo sapiens

<400> 65

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ctgcttttta ttattcctgg ttggattgca ccactactca gtttctattt tataatactg	180
attataaaac atgggaggga aataactttg tattggtttt tatggataat ttattatgtg	240
tcctagactc tggccttgctc aaaagaagga cgtaagaagg cacgatgtat tataacttggg	300

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aatgatagaa gagactgacc tggatatttcc acccggaaga gggaaaggat tttaactaca 360
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gccacctctc ttccaaaaca attccttact tctgtggtct gcaaggcggg tttttgaatg 480
gaacagaaca tagtaatata ggaaaacaca atgatgagaa aagccagcaa gttcacacct 540
gttggggaaa agcacacttt taacatctca ggcgtaaaag tcaacagtaa aattactgtg 600
gtacagggtg agtatccctt acccaaaatg tttgaaacca gaaatgtttt ggatttcgga 660
tttgggaata tttacacatt cataatgata tatcttggaa atggttccca agtctaaaca 720
caaaatttat ttatgtttca tatacacctt atacacatag tctgaaagta attttgtaca 780
atattttaaa taattttggg catgaaacaa agtttgcata cattgaacca tcagacagca 840
aaagcttcag gtgtggaatt ttccacttgt ggcatcatgt tgatgctcaa aaagttccat 900
attttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960
gttaaataca gtgcctcttc cacgggcact ttcaggaagc attcttttat ataagccc 1018

```

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<210> 66
<211> 327
<212> PRT
<213> Homo sapiens

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```

<400> 66

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Tyr Ile Lys Glu Cys Phe Leu Lys Val Pro Val Glu Glu Ala Leu Tyr
1 5 10 15

```

```

Leu Thr Ser Lys Tyr Arg Leu Ser Ile Cys Asn Leu Lys Ile Gln Asn
20 25 30

```

```

Leu Lys Cys Ser Lys Ile Trp Asn Phe Leu Ser Ile Asn Met Met Pro
35 40 45

```

```

Gln Val Glu Asn Ser Thr Pro Glu Ala Phe Ala Val Trp Phe Asn Val
50 55 60

```

```

Cys Lys Leu Cys Phe Met Pro Lys Ile Ile Asn Ile Val Gln Asn Tyr
65 70 75 80

```

```

Phe Gln Thr Met Cys Ile Arg Cys Ile Asn Ile Asn Lys Phe Cys Val
85 90 95

```

```

Thr Trp Glu Pro Phe Pro Arg Tyr Ile Ile Met Asn Val Ile Phe Arg
100 105 110

```

```

Asn Pro Lys Ser Lys Thr Phe Leu Val Ser Asn Ile Leu Gly Lys Gly
115 120 125

```

```

Tyr Ser Thr Cys Thr Thr Val Ile Leu Leu Leu Thr Phe Thr Pro Glu
130 135 140

```

```

Met Leu Lys Val Cys Phe Ser Pro Thr Gly Val Asn Leu Leu Ala Phe
145 150 155 160

```

```

Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys
165 170 175

```

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Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val
180 185 190

Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys
195 200 205

Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu
210 215 220

Ile Pro Gly Gln Ser Leu Leu Ser Phe Pro Ser Ile Ile His Arg Ala
225 230 235 240

Phe Leu Arg Pro Ser Phe Asp Lys Ala Arg Val Asp Thr Ile Ile His
245 250 255

Lys Asn Gln Tyr Lys Val Ile Ser Leu Pro Cys Phe Ile Ile Ser Ile
260 265 270

Ile Lys Lys Leu Ser Ser Gly Ala Ile Gln Pro Gly Ile Ile Lys Ser
275 280 285

Arg Ser Tyr Arg Glu Thr Lys Ser Glu Tyr Leu Ala Ser Ile Ala Arg
290 295 300

His Trp Phe Phe Thr Arg Ser Met His Lys Thr Ile Lys Ile Tyr Met
305 310 315 320

Pro Arg Phe His Pro Gly Leu
325

<210> 67
<211> 1251
<212> DNA
<213> Homo sapiens

<400> 67
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gaggactcct accccaagg tggctgggac acggtcttcc tgggtggcct gctgctcctt 120
gggctgccag ccaatgggtt gatggcgtgg ctggccggct cccaggcccg gcatggagct 180
ggcaegcgtc tggcgctgct cctgctcagc ctggccctct ctgacttctt gttcctggca 240
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gcctgccgct tctactactt cctatggggc gtgtcctact cctccggcct ctccctgctg 360
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cgcccagtcc gcctgccctt ctgggtctgc gccggtgtct ggggtgctggc cacactcttc 480
agcgtgccct ggctggtctt ccccaggct gccgtctggt ggtacgacct ggtcatctgc 540
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tgccaccgcc aacagcagcc cgcagcctgc cggggcttcg cccgtgtggc caggaccatt 720
ctgtcagcct atgtggtcct gaggctgcc taccagctgg cccagctgct ctacctggcc 780
ttcctgtggg acgtctactc tggctacctg ctctgggagg ccctggtcta ctccgactac 840

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ctgatcctac tcaacagctg cctcagcccc ttctcttgcc tcatggccag tgccgacctc 900
cggaccctgc tgcgctccgt gctctcgctc ttgcgggcag ctctctgcga ggagcggccg 960
ggcagcttca cgcccactga gccacagacc cagctagatt ctgagggtcc aactctgcca 1020
gagccgatgg cagaggccca gtcacagatg gatcctgtgg cccagcctca ggtgaacccc 1080
aactccagc cagcatcgga tcccacagct cagccacagc tgaaccctac ggcccagcca 1140
cagtcggatc ccacagccca gccacagctg aacctcatgg cccagccaca gtcagattct 1200
gtggcccagc cacaggcaga cactaacgtc cagaccctg cacctgctgc c 1251

```

<210> 68
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 68

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Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro Arg Thr
1          5          10          15
Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp Thr Val
20        25        30
Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro Ala Asn Gly Leu Met
35        40        45
Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr Arg Leu
50        55        60
Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe Leu Ala
65        70        75        80
Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His Trp Pro
85          90          95
Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly Val Ser
100        105        110
Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp Arg Cys
115        120        125
Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro Val Arg
130        135        140
Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr Leu Phe
145        150        155        160
Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp Tyr Asp
165        170        175
Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser Leu Arg
180        185        190
Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu Val
195        200        205
Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His Arg Gln
210        215        220
Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile

```

225		230		235		240
Leu Ser Ala Tyr	Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu					
	245			250		255
Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp						
	260			265		270
Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu						
	275			280		285
Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu						
	290			295		300
Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro						
305		310		315		320
Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly						
	325			330		335
Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro						
	340			345		350
Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro						
	355			360		365
Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro						
	370			375		380
Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser						
385		390		395		400
Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala						
	405			410		415
Ala						

<210> 69
 <211> 659
 <212> DNA
 <213> Homo sapiens

<400> 69
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 catctagtac cgctgccacc accccacaca cctgtcagca gtcgtgtgtc ctgctctggg 120
 ccctgtccct gctgcagagc atcctggaat ggatgttctg tggcttcctg tctagtgggtg 180
 ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg atttttttat 240
 gtgtgggttct ctgcggtgcc agcccggttc tgctggtcag gatcccttgt ggatcccgga 300
 agatgccctt gaccaggctg tacatgacca tccctgtcag agtgetgggc ttccctcctct 360
 gtgacctgcc ctttggcatt cagtgattcc tatttttctg gatccacgtg gatttgtcac 420
 gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaacc cattatttac 480
 ttcttcatgg gctccttttag gcagcttcaa aacaggaaga ctctctagct ggttctccag 540
 agggctctgc aggacacgcc tgagggtggaa gaaggcagat ggcggctttc tgaggaaacc 600
 ctggagctgt catgaagcag attggggcca tgaggaagag cctctgccct gtcagtcag 659

<210> 70
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val
 1 5 10 15

His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val
 20 25 30

Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser
 35 40 45

Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe
 50 55 60

Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val
 65 70 75 80

Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val
 85 90 95

Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys
 100 105 110

Trp Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr
 115 120 125

Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe
 130 135 140

Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met
 145 150 155 160

Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln
 165 170 175

Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu
 180 185 190

Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala
 195 200 205

Ser Ala Leu Ser Val
 210

<210> 71
 <211> 559
 <212> DNA
 <213> Homo sapiens

<400> 71

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gccccgggggt gggggccgct gggggcctcg ctccaccgc agcagcagca taaggctggc 120

cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgctccg 180

gcacaagtgg cggctgggct ccccgaagaa ctgggtgcag gcgccgctga gcagcaggtg 240

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 caggagactc aggcccacga tgtagcagaa gaagcgcagc gttgccaggc tggctctgcac 420
 gaagccccggg aagtccagcc ggccttgag caagtcgggg acgatggcca ccatgtggca 480
 gccaaaggaag atgagatccg cgcaggccac gtccaggagg tagatggcga aagggtttct 540
 gtagacattg gagctgagc 559

<210> 72
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 72

Leu Ser Ser Asn Val Tyr Arg Asn Pro Phe Ala Ile Tyr Leu Leu Asp
 1 5 10 15

Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile
 20 25 30

Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln
 35 40 45

Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser
 50 55 60

Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro
 65 70 75 80

Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys
 85 90 95

Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Thr Thr Cys Val
 100 105 110

Cys Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser
 115 120 125

Gly Ala Cys Thr Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly
 130 135 140

Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val
 145 150 155 160

Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu
 165 170 175

Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe
 180 185 190

Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys
 195 200 205

Leu Arg His
 210

<210> 73
 <211> 1008
 <212> DNA

<213> Homo sapiens

<400> 73

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 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttgggtgtggc catctctggc 180
 ctactcacag accagctctc cagcccttct cggccacac agaagaccct gtgcagcctg 240
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 aagatggaac atgcaggagc catggctgga gggtatcgat cccacaggac tcccagcgac 660
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 ttccttatca ctggcattgt gcaggtggcc tgccaggagt gtcacctcta cctagtgtg 780
 gaacggtacc tgtggctgct cggcgtgggc aactccctgc tcaaccact catctatgcc 840
 tattggcaga aggaggtgcy actgcagctc taccacatgg ccctaggagt gaagaaggty 900
 ctcacctcat tctctctctt tctctcggcc aggaattgtg gccagagag gccagggaa 960
 agttcctgtc acatcgtcac tatctccagc tcagagtttg atggctaa 1008

<210> 74

<211> 335

<212> PRT

<213> Homo sapiens

<400> 74

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
 1 5 10 15
 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 20 25 30
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
 145 150 155 160
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
 165 170 175
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
 180 185 190
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
 195 200 205
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300
 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
 305 310 315 320
 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
 325 330 335

<210> 75
 <211> 2137
 <212> DNA
 <213> Homo sapiens

<400> 75
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 aagcgttgca tcctgttacc tggagaccct ctgagctctc acctgctact tctgccgctg 180
 cttctgcaca gagccccggc gaggaccctt ccaggatgca ggtcccgaac agcaccggcc 240
 cggacaacgc gacgtgcag atgtgcgga acccgcgat cgcggtggcc ctgcccgtgg 300
 tgtactcgct ggtggcggcg gtcagcatcc cgggcaacct cttctctctg tgggtgctgt 360
 gccggcgcat ggggccaga tccccgtcgg tcattctcat gatcaacctg agcgtcacgg 420
 acctgatgct ggccagcgtg ttgcctttcc aaatctacta ccattgcaac cgccaccact 480

ggggtattcgg ggtgctgctt tgcaacgtgg tgaccgtggc cttttacgca aacatgtatt 540
 ccagcatcct caccatgacc tgtatcagcg tggagcgctt cctggggggtc ctgtaccgcg 600
 tcagctccaa gcgctggcgc cgcctgctgt acgcgggtggc cgcgtgtgca gggacctggc 660
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 ccctgggcat catcacctgc ttgcagctcc tcaagtggac gatgctcccc agcgtggcca 780
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 tttttagtag agctgggctg tcacccccga gctccttaga cactectcac acctgtccat 1680
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 gcccggtgca cgcggaaatt tctgtttatt tcaactcagg gcactgtggt tgetgtggtt 2040
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<210> 76
 <211> 359
 <212> PRT
 <213> Homo sapiens
 <400> 76

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met

1 5 10 15
 Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
 20 25 30
 Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
 35 40 45
 Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
 50 55 60
 Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
 65 70 75 80
 Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
 85 90 95
 Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
 100 105 110
 Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
 115 120 125
 Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
 130 135 140
 Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg
 145 150 155 160
 Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
 165 170 175
 Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
 180 185 190
 Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
 195 200 205
 Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
 210 215 220
 Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
 225 230 235 240
 Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
 245 250 255
 Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
 260 265 270
 His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300
 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335
 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350

Gln Arg Gln Glu Ser Val Phe
355

<210> 77
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 77
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gtggtgtgcc tggcgggtgtg cgccttcctc gtgctagaga atctagccgt gttgttggtg 180
ctcggacgcc acccgcgctt ccacgctccc atgttcctgc tcctgggcag cctcacgttg 240
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gcgtccgtgc tgagcctcct ggccatcgcg ctggagcgca gcctcaccat ggcgcgcagg 420
gggccgcgc cgtctccag tcggggggcg acgctggcga tggcagccgc ggcctggggc 480
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ttcgtgggca tcctggccgc tatctgtgca ctctacgcgc gcactactg ccaggtacgc 660
gccaacgcgc ggcgcctgcc ggcacggccc gggactgcgg ggaccacctc gaccggggcg 720
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ctgaaccca tcatctacac gctcaccaac cgcgacctgc gccacgcgt cctgcgcctg 960
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gcggctgagg cttccggggg cctgcgccgc tgccctgccc cgggccttga tgggagcttc 1080
agcggctcgg agcgtctatc gccccagcgc gacgggctgg acaccagcgg ctccacaggc 1140
agccccggtg caccacagc cgccccgact ctggtatcag aaccggctgc agactga 1197

<210> 78
<211> 398
<212> PRT
<213> Homo sapiens

<400> 78
Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
1 5 10 15
Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
20 25 30
Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60
 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80
 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
 85 90 95
 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
 100 105 110
 Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
 115 120 125
 Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140
 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160
 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175
 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190
 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205
 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
 210 215 220
 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240
 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255
 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270
 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285
 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300
 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320
 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335
 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350
 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365
 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380
 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp

385

390

395

<210> 79
 <211> 1041
 <212> DNA
 <213> Homo sapiens

<400> 79
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 tgcttccaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180
 gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 240
 tgggcttttg gggacattcc ctgccgagt gggctcttca cgttggccat gaacagggcc 300
 gggagcatcg tgttccttac ggtggaggct gcggacaggt atttcaaagt ggtccacccc 360
 caccacgcgg tgaacactat ctccaccggg gtggcggctg gcatcgtctg caccctgtgg 420
 gccctggcca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
 acggccgtct cctgtgagag cttcatcatg gactcggcca atggctggca tgacatcatg 540
 ttccagctgg agttctttat gccctcggc atcatcttat tttgctcctt caagattgtt 600
 tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgaccgg 660
 ttcatcatgg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 720
 ctctatttcc tctggacggt gccctcaggt gctcgcgac cctctgtcca tggggccctg 780
 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 840
 tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaaccaag 900
 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
 aggagttgca tcagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc 1020
 cacattgttg agtggcactg a 1041

<210> 80
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 80

Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 1 5 10 15

Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
 20 25 30

Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45

Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60

Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His

65	70	75	80
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala	85	90	95
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp	100	105	110
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser	115	120	125
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile	130	135	140
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu	145	150	155
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp	165	170	175
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile	180	185	190
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln	195	200	205
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val	210	215	220
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg	225	230	235
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val	245	250	255
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met	260	265	270
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe	275	280	285
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His	290	295	300
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg	305	310	315
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly	325	330	335
Gln Trp Asp Pro His Ile Val Glu Trp His	340	345	

<210> 81

<211> 2525

<212> DNA

<213> Homo sapiens

<400> 81

caagaatgac aggtgacttc ccaagtatgc ctggccacaa tacctccagg aattcctctt 60

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tggtgggtgt catttccatt cttttcctcc tggtgaaaat gaacaccg tcaagtacca 180

ccatggcggg	cattaacttg	gtgggtgggtcc	acagcggtttt	tctgctgaca	gtgccatttc	240
gcttgaccta	cctcatcaag	aagacttgga	tgtttgggct	gcccttctgc	aaatttgtga	300
gtgccatgct	gcacatccac	atgtacctca	cgttcctatt	ctatgtgggtg	atcctgggtca	360
ccagatacct	catcttcttc	aagtgc aaaag	acaaagtgga	attctacaga	aaactgcatg	420
ctgtgggctgc	cagtgtctggc	atgtggacgc	tgggtgattgt	cattgtggta	cccctgggtg	480
tctcccggtg	tggaatccat	gaggaataca	atgaggagca	ctgttttaaa	tttcacaaaag	540
agcttgctta	cacatatgtg	aaaatcatca	actatatgat	agtcattttt	gtcatagccg	600
ttgctgtgat	tctgttggtc	ttccaggtct	tcatcattat	gttgatgggtg	cagaagctac	660
gccactcttt	actatccac	caggagtctt	gggctcagct	gaaaaaccta	ttttttatag	720
gggtcatcct	tgtttgtttc	cttcctacc	agttcttttag	gatctattac	ttgaatgttg	780
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taacagcaat	tagctgctat	gatttgcttc	tctttgtctt	tgggggaagc	cattgggtta	900
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tcatatttgc	ttcctttata	ttgggaataa	aaatgggtat	aggggaggta	agaatggtat	1020
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agagccctca	ttgtagtcct	tatgggatcc	ctcccatctc	tgagtgatgg	ccgtacaaaag	1140
accagtgttg	ttgaatccac	ctggagtgc	aatattacat	tattttccag	tacagaatgt	1200
ctgtgtggcc	catgaaagca	acataggttt	taagagtttt	agagtttcat	tagctcattc	1260
taagtctctc	tgtttgaagc	atggtctctt	aggttttgga	ctgaactcag	acctttagtt	1320
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gataagggga	gagaatagtt	aaaaattttt	ctagggtatc	ataactctgg	taggaagtca	1500
tctgtctaga	aatcaagaga	aaaagaacgt	gtggcctcct	gttataacaa	gggtttctag	1560
at ttgtcctg	tgaagggtcg	tttaaggact	tggggatcaa	cttcctcaat	tatcaccaat	1620
tgcactgttg	ctccaaaaat	cattttaaag	cttactggac	atatctacat	aatggtgaaa	1680
ctgtaattta	gagactatcc	ctgactaatg	tgctggtagg	cattaaaatg	agttcccaag	1740
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cacagttaat	taagattttt	aggggggaca	gaaagttata	ctgaaatctt	tagagctccc	1860
ttcgcgcgtt	aaaattatat	atatatatat	ttaaattata	ccttaagttc	tggggtagat	1920
gtgcagaatg	tgcaggtttg	ttacataggt	atacagtg	catggtgggt	tgcggcacct	1980
gtcaacccat	ctacattagg	tattttctct	aatgctctcc	ctcccctagc	ccccacccc	2040
tggacaggcc	ccattgtgtg	atgttccct	ccctgtgtcc	atgtgttttc	attgttcaac	2100
tcccacttct	aagtgagaac	atgcggtgtt	tggttttctg	ttcctgtgtt	agtttgctga	2160

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gaatgatggt ttccagggtta aaattatata tttttaaata aatgaaaact gtgttttttaa 2220
aagaggactt ttgagaagta tatagaaaaa ccattaattt agactctgtg agattagggtt 2280
gcatgaagaa ggtttttctga atatttgaag agtggataaa taaatgtccc ccaaagcaat 2340
aaaatcataa tcctttaaaaa tataggaaaa ataactaatg ggaactaggc ttaatactcg 2400
ggatgaaata atctgtacaa caaactccca tgacacatgt ttacctatgt aacaaacctg 2460
cacatgtacc cctgaactta aaataaaatt taaagtataa taataaaata atatggattt 2520
tctttt 2525

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<210> 82
<211> 312
<212> PRT
<213> Homo sapiens

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<400> 82

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Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn
1          5          10          15
Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe
20        25        30
Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu
35        40        45
Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn
50        55        60
Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu
65        70        75        80
Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys
85        90        95
Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe
100       105       110
Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys
115      120      125
Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala
130      135      140
Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser
145      150      155      160
Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe
165      170      175
His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile
180      185      190
Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val
195      200      205
Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser
210      215      220

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His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val
 225 230 235 240

Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu
 245 250 255

Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr
 260 265 270

Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu
 275 280 285

Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly
 290 295 300

Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 83

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 83

gcaggagcac tgaaaatcag gaacaatcct gtattttttg tgataatcaa caaggacaaa 60
 acttctccat atgtaaataa cagcggtatg agcagcaatt catccctgct ggtggctgtg 120
 cagctgtgct acgcgaacgt gaatgggtcc tgtgtgaaaa tccccttctc gccgggatcc 180
 cgggtgattc tgtacatagt gtttggtctt ggggctgtgc tggtgtgtt tggaaacctc 240
 ctggtgatga tttcaatcct ccatttcaag cagctgcact ctccgaccaa ttttctcggt 300
 gcctctctgg cctgcgctga tttcttggtg ggtgtgactg tgatgccctt cagcatggtc 360
 aggacggtgg agagctgctg gtattttggg aggagttttt gtactttcca cacctgctgt 420
 gatgtggcat tttgttactc ttctctcttt cacttgtgct tcatctccat cgacaggtac 480
 attgcggtta ctgacccctt ggtctatcct accaagttca ccgtatctgt gtcaggaatt 540
 tgcacagcg tgtcctggat cctgcccctc atgtacagcg gtgctgtgtt ctacacaggt 600
 gtctatgacg atgggctgga ggaattatct gatgccctaa actgtatagg aggttgtcag 660
 accgttgtaa atcaaaactg ggtgttgaca gattttctat ccttctttat acctaccttt 720
 attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata 780
 gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg 840
 agagagagaa aagcagctaa aaccctgggg gtcacagtgg tagcatttat gatttcatgg 900
 ttaccatata gcattgattc attaattgat gcctttatgg gctttataac ccctgcctgt 960
 atttatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat 1020
 gctttatttt acccatggtt taggaaagca ataaaagtta ttgtaactgg tcaggtttta 1080
 aagaacagtt cagcaaccat gaatttgttt tctgaacata tataa 1125

<210> 84

<211> 345

<212> PRT

<213> Homo sapiens

<400> 84

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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1      5      10      15
Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
20      25      30
Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
35      40      45
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
50      55      60
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65      70      75      80
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
85      90      95
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
100     105     110
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
115     120     125
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
130     135     140
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145     150     155     160
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
165     170     175
Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr
180     185     190
Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile
195     200     205
Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala
210     215     220
Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser
225     230     235     240
Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala
245     250     255
Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu
260     265     270
Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr
275     280     285
Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser
290     295     300
Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys
305     310     315     320

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Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala
 325 330 335

Thr Met Asn Leu Phe Ser Glu His Ile
 340 345

<210> 85
 <211> 1020
 <212> DNA
 <213> Homo sapiens

<400> 85
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 gcttttgga attgcactga tgaaaacatc ccactcaaga tgcactacct ccctgttatt 120
 tatggcatta tcttctcgt gggatttcca ggcaatgcag tagtgatata cacttacatt 180
 ttcaaaatga gaccttgga gagcagcacc atcattatgc tgaacctggc ctgcacagat 240
 ctgctgtatc tgaccagcct ccccttctctg attcactact atgccagtgg cgaaaactgg 300
 atctttggag atttcatgtg taagtttata cgcttcagct tccatttcaa cctgtatagc 360
 agcatcctct tcctcacctg tttcagcatc ttccgctact gtgtgatcat tcaccaatg 420
 agctgctttt ccattcacaa aactcgatgt gcagttgtag cctgtgctgt ggtgtggatc 480
 atttcaactg tagctgtcat tccgatgacc ttcttgatca catcaaccaa caggaccaac 540
 agatcagcct gtctcgacct caccagtctg gatgaactca atactattaa gtggtacaac 600
 ctgattttga ctgcaagtac tttctgcctc cccttggtga tagtgacact ttgctatacc 660
 acgattatcc acactttgac ccattggactg caaactgaca gctgccttaa gcagaaagca 720
 cgaaggctaa ccattctgct actccttgca ttttacgtat gttttttacc ctccatatac 780
 ttgagggtca ttcaggatcg aatctcagcc tgctttcaat cagttgttcc attgagaatc 840
 agatccatga agcttacatc gtttctagac cattatgctg ctctgaacac ctttggtaac 900
 ctgttactat atgtggtggt cagcgacaac tttcagcagg ctgtctgctc aacagtgaga 960
 tgcaaagtaa gcgggaacct tgagcaagca aagaaaatta gttactcaa caacccttga 1020

<210> 86
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 86

Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
 1 5 10 15
 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
 20 25 30
 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
 35 40 45
 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
 50 55 60

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Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
 65 70 75 80
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
 100 105 110
 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125
 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140
 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
 145 150 155 160
 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
 165 170 175
 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
 180 185 190
 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys
 195 200 205
 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
 210 215 220
 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
 225 230 235 240
 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
 245 250 255
 Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln
 260 265 270
 Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu
 275 280 285
 Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val
 290 295 300
 Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys
 305 310 315 320
 Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn
 325 330 335

<210> 87

<211> 1138

<212> DNA

<213> Homo sapiens

<400> 87

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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180

aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca 240

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aagggaaaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300
taatatattcc tgtgtgaaaa acaactgggtc aaatgatgtc cgtgcttccc tgtacagttt 360
aatgggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc 420
acacttcaaaa caacttcata ccccaacaaa ttggctcatt cattccatgg ccaactgtgga 480
ctttcttctg ggggtgtctg tcatgcctta cagtatgggtg agatctgctg agcactgttg 540
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ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660
gagatataaa gccaaagatga atatcttggg tatttgtgtg atgatcttca ttagttggag 720
tgtccctgct gtttttgcac ttggaatgat ctttctggag ctaaacttca aaggcgctga 780
agagatatat tacaacatg ttcactgcag aggaggttgc tctgtcttct ttagcaaaat 840
atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt 900
ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagt atgccaatca 960
gaagctccaa attggattgg aaatgaaaaa tggaatttca caaagcaaag aaaggaaaagc 1020
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<210> 88
<211> 296
<212> PRT
<213> Homo sapiens

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<400> 88

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Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
1          5          10          15
Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20          25          30
Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35          40          45
Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50          55          60
Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65          70          75          80
Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85          90          95
Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100         105         110
His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115         120         125
Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130         135         140

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Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145 150 155 160

Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165 170 175

His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180 185 190

Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala
275 280 285

Arg Gly Ser Arg Ala Asn Ser Ala
290 295

<210> 89

<211> 1023

<212> DNA

<213> Homo sapiens

<400> 89

ggaatgatgc ccttttgcca caatataatt aatatttcct gtgtgaaaaa caactggtca 60

aatgatgtcc gtgcttccct gtacagtta atgggtgctca taattctgac cacactcggt 120

ggcaatctga tagttattgt ttctatatca cacttcaaac aacttcatac cccaacaaat 180

tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggt catgccttac 240

agtatggtga gatctgctga gcactgttgg tattttggag aagtcttctg taaaattcac 300

acaagcaccg acattatgct gagctcagcc tccattttcc atttgtcttt catctccatt 360

gaccgctact atgctgtgtg tgatccactg agatataaag ccaagatgaa tatcttggtt 420

atttgtgtga tgatcttcat tagttggagt gtccctgctg tttttgcatt tggaatgatc 480

tttctggagc taaacttcaa aggcgctgaa gagatatatt acaaacatgt tcaactgcaga 540

ggaggttgct ctgtcttctt tagcaaaata tctggggtag tgacctttat gacttctttt 600

tatatacctg gatctattat gttatgtgtc tattacagaa tatatcttat cgctaaagaa 660

caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatgaaaaat 720

ggaatttcac aaagcaaaga aaggaaagct gtgaagacat tggggattgt gatgggagtt 780

ttcctaatat gctgggtgcc tttctttatc tgtacagtca tggacccttt tcttcactac 840

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attattccac ctactttgaa tgatgtattg atttggtttg gctacttgaa ctctacattt 900
aatccaatgg tttatgcatt tttctatcct tggtttagaa aagcactgaa gatgatgctg 960
tttggtaaaa ttttccaaaa agattcatcc aggtgtaaatt tatttttgga attgagttca 1020
tag 1023

<210> 90
<211> 339
<212> PRT
<213> Homo sapiens

<400> 90

Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
1 5 10 15
Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20 25 30
Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35 40 45
Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50 55 60
Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65 70 75 80
Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85 90 95
Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100 105 110
His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115 120 125
Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130 135 140
Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145 150 155 160
Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165 170 175
His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180 185 190
Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195 200 205
Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210 215 220
Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225 230 235 240
Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245 250 255
Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val

260

265

270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val
 275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr
 290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe
 305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu
 325 330 335

Leu Ser Ser

<210> 91

<211> 1696

<212> DNA

<213> Homo sapiens

<400> 91

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 cacagcaccg tctctcccat actcggatcat tcacaccatc attgattcac caggcaccac 180
 tccgtgtcca gcaggactct ggggaccca aatggacact accatggaag ctgacctggg 240
 tgccactggc cacaggcccc gcacagagct tgatgatgag gactcctacc cccaaggtgg 300
 ctgggacacg gtcttcctgg tggccctgct gctccttggg ctgccagcca atgggttgat 360
 ggcgtggctg gccggctccc aggcccgga tggagctggc acgcgtctgg cgctgctcct 420
 gctcagcctg gccctctctg acttcttgtt cctggcagca gcggccttcc agatcctaga 480
 gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttcct 540
 atggggcgtg tctactcct cggcctctt cctgctggcc gccctcagcc tcgaccgctg 600
 cctgctggcg ctgtgccac actggtacc tgggcaccgc ccagtccgcc tgcccctctg 660
 ggtctgcgcc ggtgtctggg tgctggccac actcttcagc gtgccctggc tggctctccc 720
 cgaggctgcc gtctggtggt acgacctggt catctgcctg gacttctggg acagcgagga 780
 gctgtcgtg aggatgctgg aggtcctggg gggcttctct cctttcctcc tgctgctcgt 840
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 agcctgccgg ggcttcgccc gtgtggccag gaccattctg tcagcctatg tggctctgag 960
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acagatggat cctgtggccc agcctcaggt gaaccccaca ctccagccac gatcggatcc 1320
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acagctgaac ctcatggccc agccacagtc agattctgtg gccagccac aggcagacac 1440
taacgtccag acccctgcac ctgctgccag ttctgtgccc agtcctctgtg atgaagcttc 1500
cccaacccca tctctgcata ctaccccagg ggcccttgag gaccagcca cacctcctgc 1560
ctctgaagga gaaagcccca gcagaccccc gccagaggcg gcccggggcg caggcccccac 1620
gtgagggtcc aggaacacgc aggcccacca gagcagtga agagcccagg gcagacagag 1680
gaaccagcca gtcaga 1696

<210> 92
<211> 505
<212> PRT
<213> Homo sapiens

<400> 92

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Thr Ile Ile Asp Ser Pro Gly Thr Thr Pro Cys Pro Ala Gly Leu Trp
20 25 30
Gly Pro Gln Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly
35 40 45
His Arg Pro Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly
50 55 60
Gly Trp Asp Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro
65 70 75 80
Ala Asn Gly Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly
85 90 95
Ala Gly Thr Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp
100 105 110
Phe Leu Phe Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His
115 120 125
Gly Gly His Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe
130 135 140
Leu Trp Gly Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu
145 150 155 160
Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly
165 170 175
His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val
180 185 190
Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala
195 200 205
Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu
210 215 220

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Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe
225 230 235 240

Leu Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg
245 250 255

Thr Cys His Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg
260 265 270

Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr
275 280 285

Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser
290 295 300

Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu
305 310 315 320

Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp
325 330 335

Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu
340 345 350

Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln
355 360 365

Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln
370 375 380

Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln
385 390 395 400

Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln
405 410 415

Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln
420 425 430

Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln
435 440 445

Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala
450 455 460

Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro
465 470 475 480

Ala Thr Pro Pro Ala Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro
485 490 495

Glu Ala Ala Pro Gly Ala Gly Pro Thr
500 505

<210> 93

<211> 1413

<212> DNA

<213> Homo sapiens

<400> 93

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gatgatgagg actcctaccc ccaaggtggc tgggacacgg tcttcctggt ggccctgctg 120

ctccctgggc tgccagccaa tgggttgatg gcgtggctgg ccggctccca ggcccgcat 180
 ggagctggca cgcgtctggc gctgctcctg ctacgcctgg ccctctctga cttcttggtc 240
 ctggcagcag cggccttcca gatccatagag atccggcatg ggggacactg gccgctgggg 300
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 ctgctggccg ccctcagcct cgaccgctgc ctgctggcgc tgtgcccaca ctggtaccct 420
 gggcaccgcc cagtccgcct gccctctgg gtctgcgccg gtgtctgggt gctggccaca 480
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 atctgcctgg acttctggga cagcgaggag ctgtcgtga ggatgctgga ggtcctgggg 600
 ggcttctgc ctttctcct gctgctcgtc tgccacgtgc tcaccaggc cacagcctgt 660
 cgcacctgcc accgccaaca gcagcccgca gcctgccggg gcttcgccg tgtggccagg 720
 accattctgt cagcctatgt ggtcctgagg ctgccctacc agctggccca gctgctctac 780
 ctggccttcc tgtgggacgt ctactctggc tacctgctct gggaggccct ggtctactcc 840
 gactacctga tctactcaa cagctgcctc agcccttcc tctgcctcat ggccagtgcc 900
 gacctccgga cctgctgcg ctccgtgctc tcgtccttcg cggcagctct ctgcgaggag 960
 cggccgggca gcttcacgcc cactgagcca cagaccagc tagattctga gggccaact 1020
 ctgccagagc cgatggcaga gggccagtca cagatggatc ctgtggccca gcctcagggtg 1080
 aacccacac tccagccacg atcgatccc acagctcagc cacagctgaa ccctacggcc 1140
 cagccacagt cggatccac agccagcca cagctgaacc tcatggccca gccacagtca 1200
 gactctgtgg cccagccaca ggcagacact aacgtccaga cccctgcacc tgctgccagt 1260
 tctgtgccca gtcctgtga tgaagcttc ccaacccat cctgcctcc taccaggg 1320
 gcccttgagg accagccac acctcctgcc tctgaaggag aaagccccag cagcaccg 1380
 ccagaggcgg ccccgggcgc agggccacg tga 1413

<210> 94
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 94

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro
1 5 10 15

Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly
35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr
50 55 60

Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe

65		70		75		80									
Leu	Ala	Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His
				85					90					95	
Trp	Pro	Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly
			100					105					110		
Val	Ser	Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp
		115					120					125			
Arg	Cys	Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro
	130					135					140				
Val	Arg	Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr
145					150					155					160
Leu	Phe	Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp
				165					170					175	
Tyr	Asp	Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser
		180						185					190		
Leu	Arg	Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu
		195					200					205			
Leu	Val	Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His
	210					215					220				
Arg	Gln	Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg
225					230					235					240
Thr	Ile	Leu	Ser	Ala	Tyr	Val	Val	Leu	Arg	Leu	Pro	Tyr	Gln	Leu	Ala
				245					250					255	
Gln	Leu	Leu	Tyr	Leu	Ala	Phe	Leu	Trp	Asp	Val	Tyr	Ser	Gly	Tyr	Leu
			260					265					270		
Leu	Trp	Glu	Ala	Leu	Val	Tyr	Ser	Asp	Tyr	Leu	Ile	Leu	Leu	Asn	Ser
		275					280					285			
Cys	Leu	Ser	Pro	Phe	Leu	Cys	Leu	Met	Ala	Ser	Ala	Asp	Leu	Arg	Thr
	290					295					300				
Leu	Leu	Arg	Ser	Val	Leu	Ser	Ser	Phe	Ala	Ala	Ala	Leu	Cys	Glu	Glu
305					310				315					320	
Arg	Pro	Gly	Ser	Phe	Thr	Pro	Thr	Glu	Pro	Gln	Thr	Gln	Leu	Asp	Ser
				325					330					335	
Glu	Gly	Pro	Thr	Leu	Pro	Glu	Pro	Met	Ala	Glu	Ala	Gln	Ser	Gln	Met
			340					345					350		
Asp	Pro	Val	Ala	Gln	Pro	Gln	Val	Asn	Pro	Thr	Leu	Gln	Pro	Arg	Ser
		355					360					365			
Asp	Pro	Thr	Ala	Gln	Pro	Gln	Leu	Asn	Pro	Thr	Ala	Gln	Pro	Gln	Ser
	370					375					380				
Asp	Pro	Thr	Ala	Gln	Pro	Gln	Leu	Asn	Leu	Met	Ala	Gln	Pro	Gln	Ser
385					390				395					400	
Asp	Ser	Val	Ala	Gln	Pro	Gln	Ala	Asp	Thr	Asn	Val	Gln	Thr	Pro	Ala
				405					410					415	

Pro Ala Ala

<210> 95
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 95
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<210> 96
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 96
 ttcactcgag ttagccatca aactctgagc tggagatagt gacgatgtg 49

<210> 97
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 97
 gctcaaccca ctcatttatg cc 22

<210> 98
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 98
 aaacttctct gcccttaccg tc 22

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<221> misc_feature
<223> Novel Sequence

<400> 99
aaagcagcac cccgaatacc 20

<210> 100
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 100
catgatcaac ctgagcgtca c 21

<210> 101
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 101
ttcaaagctt atggagtcgg ggctgctg 28

<210> 102
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 102
ttcactcgag tcagtctgca gccggttctg 30

<210> 103
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
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<400> 103
gcatcctggc cgctatctgt gcaactctacg 30

<210> 104

<211> 30
 <212> DNA
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<220>
 <221> misc_feature
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<400> 104
 cgtagagtgc acagatagcg gccaggatgc

30

<210> 105
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 105
 aaccccatca tctacacgc

19

<210> 106
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc feature
 <223> Novel Sequence

<400> 106
 tgcctgtgga gccgctgg

18

<210> 107
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc feature
 <223> Novel Sequence

<400> 107
 gcataagctt ccatgtacaa cgggtcgtgc tgc

33

<210> 108
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc feature
 <223> Novel Sequence

<400> 108
gcattctaga tcagtgccac tcaacaatgt ggg 33

<210> 109
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 109
gaagcccagc actgtttacc 20

<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 110
tgaaatacct gtccgcagcc 20

<210> 111
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 111
gatcaagctt atgacaggtg acttccaag tatgc 35

<210> 112
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 112
gatcctcgag gctaacggca caaaacacaa ttcc 34

<210> 113
<211> 19
<212> DNA
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<220>
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 <223> Novel Sequence

<400> 113
 cagcccaaac atccaagtc

19

<210> 114
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 114
 accccactta atcagcctc

19

<210> 115
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
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<400> 115
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34

<210> 116
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 116
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39

<210> 117
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<400> 117
 acagccccaagccaaacac

20

<210> 118
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<400> 118
ccgcaggagc aatgaaaatc ag 22

<210> 119
<211> 19
<212> DNA
<213> Artificial Sequence

<400> 119
ctgaaagttg tcgctgacc 19

<210> 120
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Novel Sequence

<400> 120
cgattatcca cactttgacc c 21

<210> 121
<211> 25
<212> DNA
<213> Artificial Sequence

<400> 121
gcataccatg aatgagccac tagac 25

<210> 122
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc feature
<223> Novel Sequence

<400> 122
gcatctcgag tcaagggttg tttgagtaac 30

<210> 123
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> misc feature
<223> Novel Sequence

<400> 123
ctgtctctct gtcctcttcc 20

<210> 124

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 124
 gcaccgatct tcattgaatt tc 22

<210> 125
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 125
 acttcaaaca acttcatacc cc 22

<210> 126
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 126
 acacacagca tagtagcg 18

<210> 127
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 127
 cagagcttga tgatgaggac 20

<210> 128
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 128
cccataggaa gtagtagaag 20

<210> 129
<211> 9
<212> PRT
<213> Synthetic substrate peptide

<220>
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<400> 129

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<210> 130
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<220>
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<220>
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<223> Novel Sequence

<400> 131
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<210> 132
<211> 48
<212> DNA
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<400> 132
gcgtaatacg actcactata gggagacctg ccacactgat gcaactcc 48

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 133
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<210> 134
<211> 50
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<400> 134
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<210> 135
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<220>
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<400> 135
gcacaaaaca caattccata agcc 24

<210> 136
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<220>
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<400> 136
gcgtaatacg actcactata gggagaccgc acaaaacaca attccataag cc 52

<210> 137
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<400> 137
gctacgccac tctttactat ccc 23

<210> 138
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<220>
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<400> 138
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<210> 139
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<220>
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<400> 139
cacacccacc aagaaatcag 20

<210> 140
<211> 48
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<220>
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<400> 140
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<400> 141
ttatgagcag caattcatcc c 21

<210> 142
<211> 49
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<400> 142
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<210> 143
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<213> Artificial Sequence

<220>
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<400> 143
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19

<210> 144
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<220>
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<400> 144
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<210> 145
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<400> 145
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21

<210> 146
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<400> 146
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<220>
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<400> 147
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19

<210> 148
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<220>
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<400> 148
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<210> 149
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<400> 149
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<210> 150
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<220>
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<400> 150
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<210> 151
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<220>
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 <223> Novel Sequence

<400> 151
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<210> 152
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<220>
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<400> 152
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<400> 153
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<220>
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<400> 154
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<210> 155
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<220>
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<400> 155
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<210> 156
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<210> 157
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<220>

<221> misc_feature

<223> Novel Sequence

<400> 157

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35

<210> 158

<211> 31

<212> DNA

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<221> misc_feature

<223> Novel Sequence

<400> 158

gatcctcgag tcacgtgggg cctgcgcccg g

31

<210> 159

<211> 52

<212> DNA

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<400> 159

gcgtaatacg actcactata gggagaccgc gtgtctgcta gactctattt cc

52

<210> 160

<211> 20

<212> DNA

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<220>

<221> misc_feature

<223> Novel Sequence

<400> 160

tgccacactg atgcaactcc

20

<210> 161

<211> 48

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<220>

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<400> 161

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48

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<400> 162
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24

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50

<210> 164
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<400> 164
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24

<210> 165
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<400> 165
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52

<210> 166
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<220>
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<223> Novel Sequence

<400> 166

gctacgccac tctttactat ccc

23

<210> 167

<211> 49

<212> DNA

<213> Artificial Sequence

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49

<210> 168

<211> 20

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<213> Artificial Sequence

<220>

<221> misc_feature

<223> Novel Sequence

<400> 168

cacacccacc aagaaatcag

20

<210> 169

<211> 48

<212> DNA

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<220>

<221> misc_feature

<223> Novel Sequence

<400> 169

gcgtaatacg actcactata gggagaccca caccaccaa gaaatcag

48

<210> 170

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Novel Sequence

<400> 170

ttatgagcag caattcatcc c

21

<210> 171

<211> 49

<212> DNA
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<400> 171
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<400> 172
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<210> 173
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<400> 173
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<220>
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<400> 174
 cgattatcca cactttgacc c 21

<210> 175
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<400> 175

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<210> 176
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<400> 176
 agaagacaga gcaacctcc 19

<210> 177
 <211> 47
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<220>
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<400> 177
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<210> 178
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 <212> DNA
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<220>
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<400> 178
 ctgtaaaatt cacacaagca cc 22

<210> 179
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<400> 179
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<210> 180
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<400> 180
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<400> 181
acagcccaa agccaaacac 20

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<400> 182
ccgcaggagc aatgaaaatc ag 22

<210> 183
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<220>
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<400> 183
ctgtctctct gtcctcttcc 20

<210> 184
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<220>
<221> misc feature
<223> Novel Sequence

<400> 184
gcaccgatct tcattgaatt tc 22

<210> 185

<211> 1188
 <212> DNA
 <213> Homo sapiens

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 ctatccaacg cactgggtgct gctttgttgc gcctacagcg ctgagctccg cactcgagcc 180
 tcaggcgctcc tcctgggtgaa tctgtctctg ggccacctgc tgctggcggc gctggacatg 240
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<210> 186
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 186
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 20 25 30
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
 35 40 45
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
 50 55 60

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Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65 70 75 80
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
 85 90 95
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
 100 105 110
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
 115 120 125
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
 130 135 140
 Ser Trp Leu Gly Tyr Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
 145 150 155 160
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
 165 170 175
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
 180 185 190
 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
 195 200 205
 Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val
 210 215 220
 Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
 225 230 235 240
 Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
 245 250 255
 Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
 260 265 270
 Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
 275 280 285
 Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
 290 295 300
 Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
 305 310 315 320
 Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
 325 330 335
 Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp
 340 345 350
 Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His
 355 360

<210> 187

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<221> misc feature

<223> Novel Sequence

<400> 187
gcataagctt gccatgggcc ccggcgagg 29

<210> 188
<211> 28
<212> DNA
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<400> 188
gcattctaga cctcagtgtg tctgctgc 28

<210> 189
<211> 20
<212> DNA
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<223> Novel Sequence

<400> 189
tgctgctttg ttgcgcctac 20

<210> 190
<211> 18
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<400> 190
ttggacgcca ggaaggtg 18

<210> 191
<211> 1644
<212> DNA
<213> Homo sapiens

<400> 191
actaactttg ggaactcgta tagaccagc gtcgctcccc gcgcgcctc gcctccactt 60
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tgggctgggg tctcaacctg accttggggc aaggagcccc tgcctctggg ccgcccagcc 240
cgctgctggg ggcacggcgc tgtcacagct ggcctgggaa ctgctgggag agccccgcgc 300
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ctcgcccccac ctagtggtgc tcatcgccct cgagcgccgg cgcgcggtgc gtcttccgca 420
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ggcgtgccc ccggccttcg tggtgcgcg ggactcccc tcgccgctgc cgccgcgcc 540
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gcttgccccc accccctcc cgcccagac cctgccttg ctctgcgaa agtgccttct 1260
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aggcctgcca gggctctgtc agatcacaag gggcaggaga gtctgtgaga gagtgcact 1380
gaagttgtcc ccttctcca ctctctatt cccttctcat gtttacattt ccctatgctc 1440
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cactggaaag ttgtaaaaac aaaaacagtt atttttgag ttttcttca cgcatttata 1560
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atcatctgta tttacttatt ttga 1644

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<210> 192
<211> 513
<212> PRT
<213> Homo sapiens

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<400> 192
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Met Glu Asp Leu Phe Ser Pro Ser Ile Leu Pro Pro Ala Pro Asn Ile
1           5           10           15

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Ser Val Pro Ile Leu Leu Gly Trp Gly Leu Asn Leu Thr Leu Gly Gln
20           25           30

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Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val Phe
35           40           45

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Leu Gly Val Ile Leu Val Val Ala Val Ala Gly Asn Thr Thr Val Leu
50           55           60

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Cys Arg Leu Cys Gly Gly Gly Gly Pro Trp Ala Gly Pro Lys Arg Arg
 65 70 75 80
 Lys Met Asp Phe Leu Leu Val Gln Leu Ala Leu Ala Asp Leu Tyr Ala
 85 90 95
 Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala Trp Glu Leu Leu Gly Glu
 100 105 110
 Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys Arg Phe Leu Gln Leu Leu
 115 120 125
 Gln Ala Ser Gly Arg Gly Ala Ser Ala His Leu Val Val Leu Ile Ala
 130 135 140
 Leu Glu Arg Arg Arg Ala Val Arg Leu Pro His Gly Arg Pro Leu Pro
 145 150 155 160
 Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu Leu Ala Leu Leu Leu Ala
 165 170 175
 Leu Pro Pro Ala Phe Val Val Arg Gly Asp Ser Pro Ser Pro Leu Pro
 180 185 190
 Pro Pro Pro Pro Pro Thr Ser Leu Gln Pro Gly Ala Pro Pro Ala Ala
 195 200 205
 Arg Ala Trp Pro Gly Glu Arg Arg Cys His Gly Ile Phe Ala Pro Leu
 210 215 220
 Pro Arg Trp His Leu Gln Val Tyr Ala Phe Tyr Glu Ala Val Ala Gly
 225 230 235 240
 Phe Val Ala Pro Val Thr Val Leu Gly Val Ala Cys Gly His Leu Leu
 245 250 255
 Ser Val Trp Trp Arg His Arg Pro Gln Ala Pro Ala Ala Ala Ala Pro
 260 265 270
 Trp Ser Ala Ser Pro Gly Arg Ala Pro Ala Pro Ser Ala Leu Pro Arg
 275 280 285
 Ala Lys Val Gln Ser Leu Lys Met Ser Leu Leu Leu Ala Leu Leu Phe
 290 295 300
 Val Gly Cys Glu Leu Pro Tyr Phe Ala Ala Arg Leu Ala Ala Ala Trp
 305 310 315 320
 Ser Ser Gly Pro Ala Gly Asp Trp Glu Gly Glu Gly Leu Ser Ala Ala
 325 330 335
 Leu Arg Val Val Ala Met Ala Asn Ser Ala Leu Asn Pro Phe Val Tyr
 340 345 350
 Leu Phe Phe Gln Ala Gly Asp Cys Trp Leu Arg Arg Gln Leu Arg Lys
 355 360 365
 Arg Leu Gly Ser Leu Cys Cys Ala Pro Gln Gly Gly Ala Glu Asp Glu
 370 375 380
 Glu Gly Pro Arg Gly His Gln Ala Leu Tyr Arg Gln Arg Trp Pro His
 385 390 395 400
 Pro His Tyr His His Ala Arg Arg Glu Pro Ala Gly Arg Gly Arg Leu
 405 410 415

Ala Pro Thr Pro Ser Ala Pro Gln Thr Pro Ala Leu Leu Leu Arg Lys
 420 425 430
 Cys Leu Leu Gly Ala Trp Trp Ser Glu Thr Gly His Leu Ser Leu Arg
 435 440 445
 Arg Asn Leu Gln Gly Thr Arg Gly Leu Pro Gly Ser Val Gln Ile Thr
 450 455 460
 Arg Gly Arg Arg Val Cys Glu Arg Val Thr Leu Lys Leu Ser Pro Ser
 465 470 475 480
 Ser Thr Leu Leu Phe Pro Ser His Val Tyr Ile Ser Leu Cys Ser Ser
 485 490 495
 Ser Phe Ser Ser Ser Leu Gln Phe Leu Ser Tyr Leu Pro Ile Trp Arg
 500 505 510
 Gln